

- 1 -

## SEQUENCE LISTING

<110> The Scripps Research Institute  
Friedlander, Martin  
Otani, Atsushi  
DaSilva, Karen

<120> HEMATOPOIETIC STEM CELLS AND METHODS OF  
TREATMENT OF NEOVASCULAR EYE DISEASES THEREWITH

<130> TSRI-900.1

<150> 60/467051  
<151> 2003-05-02

<150> 60/398522  
<151> 2002-07-25

<160> 2

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 4742  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> DNA encoding His-tagged human T2-TrpRS

<400> 1  
tggcgaatgg gacgcgcctt gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg 60  
cagcgtgacc gctacacttg ccagcgcctt agcgcgcgt ctttcgcctt tcttcgccttc 120  
ctttctcgcc acgttcgcgg gctttccccg tcaagctcta aatcggggggc tcccttttagg 180  
gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgatttagg gtgatggttc 240  
acgtatggg ccatcgccct gatagacggt ttttcgcctt ttgacgttgg agtccacgtt 300  
ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggcttattc 360  
ttttgattta taagggattt tgccgatttc ggcttattgg ttaaaaaatg agctgattta 420  
acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480  
tcggggaaat gtgcgcggaa cccctatttg tttattttc taaatacatt caaatatgtt 540  
tccgctcatg agacaataac cctgataaaat gcttcaataa tattgaaaaa ggaagagtat 600  
gagtattcaa cattccgtg tcggccttat tccctttttt gcggcatttt gccttcctgt 660  
ttttgctcac ccagaacacgc tggtaaaagt aaaagatgct gaagatcagt tgggtgcacg 720  
agtgggttac atcgaactgg atctcaacag cggttaagatc cttgagagtt ttcccccga 780  
agaacgtttt ccaatgatga gcactttaa agttctgcta tgtggcgcgg tattatcccgg 840  
tattgacgcc gggcaagagc aactcggtcg cccgatacac tattctcaga atgacttgg 900  
tgagttactca ccagtcacag aaaagatct tacggatggc atgacagtaa gagaattatg 960  
cagtgcgtcc ataaccatga gtgataaacac tgccggcaac ttacttctga caacgatcgg 1020  
aggaccgaag gagctaaccg ctttttgca caacatgggg gatcatgtaa ctcgccttga 1080  
tcgttggaa ccggagctga atgaagccat accaaacgac gagcgtgaca ccacgatgcc 1140  
tgcagcaatg gcaacaacgt tgcgcaaaactt attaactggc gaactactta ctctagcttc 1200

ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac ttctgcgctc 1260  
ggcccttcgg gctggctgg ttattgtcg taaatctgg gcccgtgagc gtgggtctcg 1320  
cggtatcatt gcagcaactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac 1380  
gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc 1440  
actgattaag cattgttaac tgtcagacca agttactca tatatacttt agattgattt 1500  
aaaacttcat tttaattta aaaggatcta ggtgaagatc cttttgata atctcatgac 1560  
caaataccct taacgtgagt ttgcgttcca ctgagcgtca gaccccgtag aaaagatcaa 1620  
aggatcttct tgagatcctt ttttctgc cgtaatctgc tgcttgaaa caaaaaaacc 1680  
accgctacca gcggtgggtt gtttgcggg tcaagagcta ccaactctt ttccgaaggt 1740  
aactggcttc agcagagcgc agataccaaa tactgtcctt ctatgttagc cgtagttagg 1800  
ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgtcaa tcctgttacc 1860  
agtggctgct gccagtggcg ataagtctg tcttaccggg ttggactcaa gacgatagtt 1920  
accggataag gcgcagcggt cgggctgaac ggggggttcg tgcacacagc ccagcttgg 1980  
gcgaacgacc tacaccgaac tgagataacct acagcgtgag ctatgagaaa gcccacgct 2040  
tcccgaaggg agaaaaggcgg acaggtatcc ggtaaagcggc agggtcggaa caggagagcg 2100  
cacgagggag cttccagggg gaaacgcctg gtatctttat agtccctgtcg ggtttcgcca 2160  
cctctgactt gagcgtcgat ttttgtatg ctgcgtcaggg gggcggagcc tatggaaaaa 2220  
cgccagcaac gcccccttt tacgggttcc ggcctttgc tggccttttgc ctcacatgtt 2280  
ctttcctgcg ttatccccctg attctgttggta taaccgtatt accgcctttg agtgagctga 2340  
taccgctcgc cgcaagccgaa cgaccgagcg cagcgtatca gtgagcgggg aagcggaga 2400  
gcgcctgtatg cggatttttc tccttacgca tctgtgcggg atttcacacc gcatatatgg 2460  
tgcactctca gtacaatctg ctctgtatcc gcatagtttaa gccagtatac actccgctat 2520  
cgctacgtga ctgggtcatg gctgcgcctt gacaccgc gaccccgct gacgcgcct 2580  
gacgggcttg tctgtcccg gcatccgc tt acagacaagc tgtgaccgtc tccggagct 2640  
gcatgtgtca gaggtttca ccgtcatcac cgaaacgcgc gaggcagctg cggtaaagct 2700  
catcagcgtg gtcgtgaagc gattcacaga tgtctgcctg ttcatccgc tccagctcgt 2760  
tgagtttctc cagaagcgtt aatgtctggc ttctgataaa gcgggcccattg ttaagggcg 2820  
tttttcctg ttttgtcact gatgcctccg tgtaaggggg atttctgttc atggggtaa 2880  
tgataccgat gaaacgagag aggtatgtca cgatacgggt tactgtatgat gaacatgccc 2940  
ggttactgga acgttgcgtt ggtaaacaaac tggcggtatg gatgcggcg gaccagagaa 3000  
aaatcactca gggtaatgc cagcgctcg ttaatacaga tgttaggttt ccacagggt 3060  
gccagcagca tcctgcgtatc cagatccggaa acataatggt gcagggcgct gacttccgc 3120  
tttccagact ttacgaaaca cggaaaccga agaccattca tgggtttgc caggtcgcag 3180  
acgtttgcgca gcagcagtcg ctgcacgttc gctcgctat cggtgattca ttctgcta 3240  
cagtaaggca accccgccc gctagccggg tcctcaacgaa caggagcagc atcatgcgc 3300  
cccgtggcca ggacccaacg ctgcccggaa tctcgatccc gcggaaattaa tacgactcac 3360  
tatagggaga ccacaacgggt ttccctctag aaataatttt gtttaacttt aagaaggaga 3420  
tatacatatg agtcaaaaag gcatagacta cgataagctc attgttgcgtt ttggaaatgt 3480  
taaaattgac aaagagctaa taaaccgaat agagagagcc accggccaaa gaccacacca 3540  
cttcctgcgc agaggcatct tcttctcaca cagagatatg aatcaggatcc ttgtatgccta 3600  
tgaaaataag aagccatttt atctgtacac gggccggggc ccctcttcgt aagcaatgca 3660  
tgttaggtcact ctcattccat ttattttcact aaagtggctc caggatgtat ttaacgtgcc 3720  
cttggtcact cagatgacgg atgacgagaa gtatctgtgg aaggacgtca ccctggacca 3780  
ggcctatggc gatgtgttg agaatgcca ggacatcatc gcctgtggct ttgacatcaa 3840  
caagactttc atattctctg acctggacta catggggatg agtcagggtt tctacaaaaa 3900  
tgtggtaag attcaaaaacg atgttacctt caaccaagtgg aaaggcattt tcggcttcac 3960  
tgacagcgcac tgcattggaa agatcaggatcc tcctgcctatc caggctgctc ctccttcag 4020  
caactcatcc ccaacagatct tcggagacag gacggatatc cagtgccatc tcccatgtgc 4080  
cattgaccag gatcctact tttagaatgac aaggagcgtc gccccccagga tcggctatcc 4140  
taaaccagcc ctgtgcact ccaccttcc cccagccctg caggccgcggcc agacaaaaat 4200  
gagtgcgcagc gacccaaact ctcctatcc ctcaccgac acggccaaagc agatcaaaaac 4260  
caaggtcaat aagcatgcgt tttctggagg gagagacacc atcgaggagc acaggcagtt 4320  
tggggcaac tgtatgtgg acgtgtctt catgtacgtt accttcttcc tcgaggacga 4380

cgacaagctc gaggcagatca ggaaggatta caccagcgga gccatgctca ccggtgagct 4440  
caagaaggca ctcatacgagg ttctgcagcc cttgatcgca gagcaccagg cccggcgcaa 4500  
ggaggtcacg gatgagatag tgaaagagtt catgactccc cggaagctgt cttcgactt 4560  
tcagaagctt gcggccgcac tcgagcacca ccaccaccac cactgagatc cggtgctaa 4620  
caaagccgaa aagaagctg agttggctgc tgccaccgct gagcaataac tagcataacc 4680  
ccttggggcc tctaaacggg tcttgagggg tttttgctg aaaggaggaa ctatatccgg 4740  
at 4742

<210> 2

<211> 392

<212> PRT

<213> Artificial Sequence

<220>

<223> His-tagged human T2-TrpRS

<400> 2

Met	Ser	Ala	Lys	Gly	Ile	Asp	Tyr	Asp	Lys	Leu	Ile	Val	Arg	Phe	Gly
1					5					10				15	
Ser	Ser	Lys	Ile	Asp	Lys	Glu	Leu	Ile	Asn	Arg	Ile	Glu	Arg	Ala	Thr
								20		25				30	
Gly	Gln	Arg	Pro	His	His	Phe	Leu	Arg	Arg	Gly	Ile	Phe	Phe	Ser	His
							35		40				45		
Arg	Asp	Met	Asn	Gln	Val	Leu	Asp	Ala	Tyr	Glu	Asn	Lys	Lys	Pro	Phe
						50		55				60			
Tyr	Leu	Tyr	Thr	Gly	Arg	Gly	Pro	Ser	Ser	Glu	Ala	Met	His	Val	Gly
					65		70			75				80	
His	Leu	Ile	Pro	Phe	Ile	Phe	Thr	Lys	Trp	Leu	Gln	Asp	Val	Phe	Asn
						85			90				95		
Val	Pro	Leu	Val	Ile	Gln	Met	Thr	Asp	Asp	Glu	Lys	Tyr	Leu	Trp	Lys
						100			105				110		
Asp	Leu	Thr	Leu	Asp	Gln	Ala	Tyr	Gly	Asp	Ala	Val	Glu	Asn	Ala	Lys
						115		120				125			
Asp	Ile	Ile	Ala	Cys	Gly	Phe	Asp	Ile	Asn	Lys	Thr	Phe	Ile	Phe	Ser
						130		135				140			
Asp	Leu	Asp	Tyr	Met	Gly	Met	Ser	Ser	Gly	Phe	Tyr	Lys	Asn	Val	Val
						145		150			155			160	
Lys	Ile	Gln	Lys	His	Val	Thr	Phe	Asn	Gln	Val	Lys	Gly	Ile	Phe	Gly
						165			170			175			
Phe	Thr	Asp	Ser	Asp	Cys	Ile	Gly	Lys	Ile	Ser	Phe	Pro	Ala	Ile	Gln
						180		185				190			
Ala	Ala	Pro	Ser	Phe	Ser	Asn	Ser	Phe	Pro	Gln	Ile	Phe	Arg	Asp	Arg
						195		200				205			
Thr	Asp	Ile	Gln	Cys	Leu	Ile	Pro	Cys	Ala	Ile	Asp	Gln	Asp	Pro	Tyr
						210		215			220				
Phe	Arg	Met	Thr	Arg	Asp	Val	Ala	Pro	Arg	Ile	Gly	Tyr	Pro	Lys	Pro
						225		230			235			240	
Ala	Leu	Leu	His	Ser	Thr	Phe	Phe	Pro	Ala	Leu	Gln	Gly	Ala	Gln	Thr
						245			250			255			
Lys	Met	Ser	Ala	Ser	Asp	Pro	Asn	Ser	Ser	Ile	Phe	Leu	Thr	Asp	Thr
						260		265				270			
Ala	Lys	Gln	Ile	Lys	Thr	Lys	Val	Asn	Lys	His	Ala	Phe	Ser	Gly	Gly
						275		280			285				

Arg Asp Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val  
290 295 300  
Asp Val Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys  
305 310 315 320  
Leu Glu Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly  
325 330 335  
Glu Leu Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu  
340 345 350  
His Gln Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe  
355 360 365  
Met Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala  
370 375 380  
Leu Glu His His His His His  
385 390